



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 151908

TO: Vanessa L Ford
Location: rem/3b25/3c18
Art Unit: 1645
Friday, April 29, 2005

Case Serial Number: 10/017168

From: Toby Port

Location: Biotech-Chem Library
REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Ford,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

STIC-Biotech/ChemLib

151906

mg

From: Chan, Christina
Sent: Wednesday, April 27, 2005 5:10 PM
To: Ford, Vanessa; STIC-Biotech/ChemLib
Subject: RE: In re: 10/017, 168 Sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
APR 28 2005
STIC-Biotech/ChemLib
(STIC)

-----Original Message-----

From: Ford, Vanessa
Sent: Wednesday, April 27, 2005 3:11 PM
To: Chan, Christina
Subject: In re: 10/017, 168 Sequence search

Please search SEQ ID NOs: 7, 8, 10, 22, 24 and 26. Please include interference searches. Please rush.

Vanessa L. Ford
Biotechnology Patent Examiner
Office: REM 3B25
Mailbox: REM 3C18
Phone: 571.272.0857
Art unit: 1645

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Cune, E.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281: 375-388, 1998

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OM protein - protein search, using SW model

Run on: April 28, 2005, 16:35:11 ; Search time 98.5021 Seconds

(without alignments)
1543.082 Million cell updates/sec

Title: US-10-017-168-26

Sequence: 1 MFVRSDFMPKNTAVEISNLE.....AVLENFQRFKDAFLKKAR 393

Scoring table:

BLOSUM62

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1364.5	68.1	312	4 AAB48318	Aab48318 T. pallid
2	1286.5	64.2	432	4 AAB48316	Aab48316 T. pallid
3	1130.5	56.4	232	4 AAB48317	Aab48317 T. pallid
4	187.5	9.4	1018	2 AAR98747	Aar98747 P. vivax
5	187.5	9.4	1018	2 AAW97039	Aaw97039 A. secreta
6	187.5	9.4	1018	4 AAG65528	Aag65528 Plasmodiu
7	187.5	9.4	1018	8 ADJ95471	Adj95471 Plasmodiu
8	182	9.1	783	2 AAR05804	Aar05804 C-termina
9	170.5	8.5	2768	4 ABB68397	Abb68397 Drosophila
10	167.5	8.4	2109	8 ADN23693	Adn23693 Bacterial
11	163	8.1	552	7 ADC31182	Adc31182 Human nov
12	162.5	8.1	1965	8 ADK47314	Adk47314 Streptococ
13	162.5	8.1	1972	6 ADK47314	Adk47314 Streptococ
14	160.5	8.0	1963	6 ABU46054	Abu46054 Protein e
15	157	7.8	1965	2 AAW69165	Aaw69165 Streptococ
16	156	7.8	278	2 AAW55109	Aaw55109 Streptococ
17	156	7.8	278	5 ABP54603	Abp54603 S. pneumo
18	156	7.8	278	7 ADC45175	Adc45175 S. pneumo
19	156	7.8	571	2 AAW5064	Aaw5064 Streptococ
20	156	7.8	571	5 ABP54558	Abp54558 S. pneumo
21	156	7.8	2004	6 ABU01577	Abu01577 S. pneumo
22	156	7.8	2004	6 ABU01577	Abu01577 S. pneumo
23	156	7.8	2004	6 ADM92167	Adm92167 S. pneumo
24	155	7.7	1000	6 ABJ25647	Abj25647 Aepexgill
25	154	7.7	795	4 ABB61567	Abb61567 Drosophila

26	152.5	7.6	486	5 AAE23036	Aae23036 Human thi
27	152	7.6	428	6 ABU44065	Abu44065 Protein e
28	151.5	7.6	2468	6 ABR64281	AbR64281 Angiogene
29	151.5	7.6	2468	7 ADE62723	Ade62723 Human Pro
30	151.5	7.6	2468	7 ADE62719	Ade62719 Human Pro
31	151.5	7.6	2468	7 ADE62727	Ade62727 Human Pro
32	151.5	7.6	2468	7 ADE62715	Ade62715 Human Pro
33	151.5	7.6	2468	8 ADL12997	Adl12997 Human ste
34	151.5	7.6	2468	8 ADN05260	Adn05260 Antipeori
35	151.5	7.6	2468	8 ADRI4614	Adri4614 Human NF-
36	151.5	7.6	2519	4 ABG16636	Abg16636 Novel hum
37	151.5	7.6	2527	8 ADN04561	Adn04561 Antipeori
38	150	7.5	522	4 AAB02397	Aae02397 Canine re
39	150	7.5	925	8 ADM97706	Adm97706 Murine MN
40	148.5	7.4	591	5 ABB92325	Abb92325 Herbicida
41	148.5	7.4	34350	8 AD089964	Ad089964 Antagonis
42	147.5	7.4	788	4 ABB68264	Abb68264 Drosophila
43	147	7.3	669	4 AAO12939	Aao12939 Human pol
44	147	7.3	905	2 AAW31186	Aaw31186 Human p16
45	147	7.3	983	8 ADM87342	Adm87342 Human pro

ALIGNMENTS

RESULT 1	
AAB48318	
ID AAB48318 standard; protein; 312 AA.	
XX	
AC AAB48318;	
XX	
DT 11-SEP-2003 (revised)	
DT 20-APR-2001 (first entry)	
XX	
DE T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).	
XX	
KM Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;	
KW yaws; bejel.	
XX	
OS Treponema pallidum; ssp. endemicum.	
XX	
PN W0200077486-A2.	
XX	
PD 21-DEC-2000.	
XX	
PF 14-JUN-2000; 2000WO-US016425.	
XX	
PR 14-JUN-1999; 99US-0138981P.	
XX	
PI (USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	
PI Liu H, Steiner B, Rhodes B;	
XX	
DR WPI: 2001-080711/09.	
DR N-PSDB; AAC84649.	
XX	
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting	
PT formation of a complex between immunogenic peptides of acidic repeat	
PT protein of the bacterium and an antibody present in the biological	
XX	
PS Claim 15; Fig 10; 73pp; English.	
XX	
CC The invention relates to a method of detecting presence of Treponema	
CC pallidum (TP), anti-treponemal antibodies (Abs), or both in a biological,	
CC sample that involves contacting an acidic repeat protein (arp), or one or	
CC more isolated immunogenic TP peptides of arp with an Ab containing	
CC immunogenic peptides and then detecting the formation of a complex between	
CC immunogenic peptides and Ab. The presence of the complex indicates the	
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,	
CC and bejel diseases. The immunogenic peptides or the Abs raised against	
CC arp, as part of an immunogenic composition, are useful for inducing a	
CC protective immune response against syphilis, yaws or bejel caused by TP.	

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OM protein - protein search, using sw model

Run on: April 28, 2005, 16:51:57 ; Search time 23.0659 Seconds
(without alignments)
1785.355 Million cell updates/sec

Title: US-10-017-168-24

Perfect score: 2180

Sequence: 1 MEVRSDMPKNTAVEISNLE.....AVLENFQRFQDAFLKKAR 428

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

P1R 79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1043.5	47.9	227 2	G71326 hypothetical prote
2	963	44.2	256 2	F71326 hypothetical prote
3	212.5	9.7	407 1	EDBEQ3 immediate-early pr
4	206.5	9.5	1271 2	A45555 glutamate rich pr
5	203	9.3	721 2	S29795 hypothetical prote
6	197.5	9.1	2109 2	E89066 protein H05009.1 f
7	197.5	9.1	2109 2	T33247 hypothetical prote
8	190.5	8.7	1110 2	I51116 NF-180 - sea lamp
9	190	8.7	630 2	S29796 hypothetical prote
10	188	8.6	544 1	I36911 involucrin L - dou
11	183.5	8.4	913 2	T52485 neurofilament prot
12	180	8.3	450 1	C29413 C29413 cytocho
13	178	8.2	391 2	S27850 surface antigen TC
14	177	8.1	7962 2	I38346 elastic titin - hu
15	176.5	8.1	1094 2	S49313 protein kinase - s
16	172	7.9	1252 2	T22523 hypothetical prote
17	170.5	7.8	1621 2	A82255 hypothetical prote
18	169	7.8	590 2	A40437 glutamic acid-rich
19	166	7.6	1963 2	B98002 IGA-specific metal
20	165.5	7.6	506 2	S47439 I2 protein - Trypa
21	165	7.6	411 2	S47436 flagellar antigen
22	164.5	7.5	5170 2	T15348 hypothetical prote
23	164	7.5	679 2	S28366 recombinaton repa
24	163	7.5	754 2	AC2807 Ompa family protei
25	163	7.5	754 2	B97586 hypothetical prote
26	161	7.4	1076 2	F96831 neurofilament trip
27	161	7.4	1020 1	QFHCH neurofilament trip
28	159.5	7.3	296 2	A54527 110k antigen - pla
29	159.5	7.3	2004 2	F95133 immunoglobulin A1

30	159	7.3	1881 2	H95076 zinc metalloprotei
31	158.5	7.3	837 2	JN0292 antigen 332 - mila
32	158.5	7.3	845 2	A45669 neurofilament trip
33	158.5	7.3	1566 2	A43607 cell surface antig
34	158	7.2	518 2	G84488 En/Spm-like transp
35	157	7.2	298 1	I36912 involucrin S - dou
36	156	7.2	849 2	S00030 neurofilament trip
37	154.5	7.1	1876 2	E97944 zinc metalloprotei
38	152.5	7.0	1560 2	T30282 calcium-binding pr
39	151.5	6.9	333 2	T10738 hypothetical prote
40	150.5	6.9	798 2	T33022 hypothetical prote
41	150.5	6.9	1087 2	T30330 gelsolin-related p
42	150	6.9	419 2	G75062 probable flagella-
43	149.5	6.9	837 2	T02761 outer arm dynein i
44	149	6.8	592 1	LBX actin-binding prot
45	149	6.8	798 2	150479 neurofilament medi

ALIGNMENTS

RESULT 1

G71326 hypothetical protein TP0434 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: G71326
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwrt
rson, J.; Knaluk, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetereback, T.; McD
tley, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A1250; MUID:98332770; PMID:9665876

A:Accession: G71326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-227 <CD>

A:Cross-references: UNIPROT:O83449; GB:AE001220; GB:AE000520; NID:g3322705; PIDN:AAC654;

A:Experimental source: strain Nichols

C:Genetics:
A:Gene: TP0434

Query Match 47.9%; Score 1043.5; DB 2; Length 227;
Best Local Similarity 91.2%; Pred. No. 1.3e-54;
Matches 207; Conservative 2; Mismatches 17; Indels 1; Gaps 1;

QY	202	REGGERVEDVPKVEPASEREGGERVEDVPKVEPASEREGGERVEDVPKVEPASE	261
DB	2	REGSVR-WRCRRYVEPASEREGGEREGCGIPKVEPASEREGGERVEDVPKVEPASEG	60
QY	262	REGGERVEDVPKVEPASEREGGERVEDVPKVEPASEREGGERVEDVPKVEPASE	321
DB	61	HEGGERVEDVPKVEPASEREGGERVEDVPKVEPASEREGGERVEDVPKVEPASE	120
QY	322	DLSESEIVPEEOKGRAPQVTPGAPRGLOPGEYVOIAVFNDAICVQSIIVHVGVEYP	381
DB	121	DLSESEIVPEEOKGRAPQVTPGAPRGLOPGEYVOIAVFNDAICVQSIIVHVGVEYP	180
QY	382	IAVEDDIHEGKVRITVCYGPVQKDERGAVLENFQRFQDAFLKKAR	428
DB	181	IAVEDDIHEGKVRITVCYGPVQKDERGAVLENFQRFQDAFLKKAR	227

RESULT 2

F71326 hypothetical protein TP0433 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: F71326
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwrt
rson, J.; Knaluk, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetereback, T.; McD
tley, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

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OM protein - protein search, using sw model

Run on: April 28, 2005, 16:35:11 ; Search time 107.275 Seconds
(without alignments)
1543.082 Million cell updates/sec

Title: US-10-017-168-24
Perfect score: 2180
Sequence: 1 MFVRSDFMPKNTAVEISNLE.....AVLENFQFGKDAFLKKAR 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1567	71.9	312	4	AAB48318
2	1475	67.7	432	4	AAB48316
3	1113	51.1	232	4	AAB48317
4	214.5	9.8	1018	2	AAB98747
5	214.5	9.8	1018	2	AAW97039
6	214.5	9.8	1018	4	AA66528
7	214.5	9.8	1018	8	ADJ95471
8	204.5	9.4	783	2	AA05804
9	201	9.2	2768	4	AAB68397
10	197.5	9.1	2109	8	ADN23693
11	192	8.8	552	7	ADG11182
12	183	8.4	1000	6	ABJ25647
13	178	8.2	486	5	ABR64281
14	178	8.2	2468	6	ABR64281
15	178	8.2	2468	7	ADG62723
16	178	8.2	2468	7	ADG62723
17	178	8.2	2468	7	ADG62727
18	178	8.2	2468	7	ADG62727
19	178	8.2	2468	8	ADG62727
20	178	8.2	2468	8	ADG62727
21	178	8.2	2468	8	ADG62727
22	178	8.2	2468	8	ADG62727
23	178	8.2	2468	8	ADG62727
24	178	8.2	2468	8	ADG62727
25	178	8.2	2468	8	ADG62727

26	171	7.8	194	4	ABG11265	Abg11265 Novel hum
27	171	7.8	522	4	AAE02397	Aae02397 Canine re
28	166	7.6	1963	6	ABU46054	Abu46054 Proteine
29	166	7.6	1965	8	ADR47314	Adr47314 Streptoco
30	166	7.6	1972	8	ADR4616	Adr4616 Novel S.
31	165.5	7.6	1428	6	ABU44065	Abu44065 Protein e
32	164.5	7.5	795	4	ABE1567	AbE1567 Drosophi
33	164	7.5	669	4	AAO12939	Aao12939 Human pol
34	164	7.5	679	4	ABE59691	AbE59691 Drosophi
35	163	7.5	489	4	ABE58655	AbE58655 Drosophi
36	162.5	7.5	615	8	ADO19437	Ado19437 Human sof
37	162.5	7.5	615	8	ABM80918	Abm80918 Tumour-a8
38	162.5	7.5	1965	2	AAW69165	Aaw69165 Streptoco
39	162	7.4	412	2	AAW03626	Aaw03626 Human thy
40	161.5	7.4	864	4	AAW39026	Aaw39026 Human pol
41	161.5	7.4	1026	4	AAW78825	Aaw78825 Human pro
42	161.5	7.4	1388	7	ADJ69333	Adj69333 Human hea
43	161	7.4	617	4	AAW16458	Aaw16458 Peptide #
44	161	7.4	617	4	ABE35445	AbE35445 Peptide #
45	161	7.4	617	4	ABE20884	AbE20884 Protein #

ALIGNMENTS

RESULT 1
ID AAB48318 standard; protein; 312 AA.
XX
AC AAB48318;
XX
DT 11-SEP-2003 (revised)
DT 20-APR-2001 (first entry)
XX
DE T. pallidum ssp. endemicum (Bosnia) acidic repeat protein (arp).
XX
KW Treponema pallidum; acidic repeat protein; arp; immunogenic; syphilis;
XX yaws; bejel.
XX
OS Treponema pallidum; ssp. endemicum.
XX
PN WO200077466-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016425.
XX
PR 14-JUN-1999; 99US-0138981P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Liu H, Steiner B, Rhodes B;
XX
DR WPI; 2001-080711/09.
XX
DE N-PSDB; AAC84645.
XX
PT Detecting Treponema pallidum in blood, saliva, etc., by detecting
PT formation of a complex between immunogenic peptides of acidic repeat
PT protein of the bacterium and an antibody present in the biological
PT sample.
XX
PS Claim 15; Fig 10; 73pp; English.
XX
CC The invention relates to a method of detecting presence of Treponema
CC pallidum (TP), anti-treponemal antibodies (Abp) or both in a biological
CC sample that involves contacting an acidic repeat protein (arp), or one or
CC more isolated immunogenic TP peptides of arp with an Ab containing
CC biological sample and then detecting the formation of a complex between
CC immunogenic peptides and Ab. The presence of the complex indicates the
CC presence of TP. The method is thus useful for diagnosing syphilis, yaws,
CC and bejel diseases. The immunogenic peptides or the Abs raised against
CC arp, as part of an immunogenic composition, are useful for inducing a
CC protective immune response against syphilis, yaws or bejel caused by TP.

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OM protein - protein search, using SW model

Run on: April 28, 2005, 16:36:51 ; Search time 81.2695 Seconds
(without alignments)
2192.749 Million cell updates/sec

Title: US-10-017-168-22
Perfect score: 1776
Sequence: 1 MFVRSDMPFKNTAVESINLE.....AVLENFORFGKAFLLKKAR 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprotc.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1776	100.0	348	2	Q9ALV7
2	1743.5	98.2	393	2	Q93CA3
3	1726	97.2	428	2	Q9ALV6
4	1656	93.2	548	2	Q93CA4
5	1043.5	58.8	432	2	Q51953
6	1042	58.7	227	2	Q83449
7	963	54.2	256	2	Q83448
8	472	26.6	458	2	Q73NG7
9	164.5	9.3	410	2	Q96214
10	163.5	9.1	1112	2	Q63G96
11	162.5	9.2	432	2	Q63G96
12	152.5	8.6	466	2	Q6NE60
13	152	8.6	614	2	Q94674
14	152	8.6	675	2	Q871R0
15	151.5	8.5	519	2	Q7S118
16	149.5	8.4	394	2	Q964D0
17	149.5	8.4	453	1	PTPI_ENGHE
18	146.5	8.2	1167	2	Q7SH54
19	145.5	8.2	1070	2	Q81YT0
20	144	8.1	687	2	Q7S7J3
21	141.5	8.0	915	2	Q6FMI8
22	140	7.9	601	2	Q711E3
23	140	7.9	3277	2	Q7NN14
24	135.5	7.6	796	2	Q96579
25	135.5	7.6	891	2	Q6NVT0
26	135.5	7.6	1964	2	Q59947
27	135	7.6	443	2	Q7D613
28	135	7.6	1963	2	Q8DPR5
29	134.5	7.5	834	2	Q91R12
30	133.5	7.5	834	2	Q71S18
31	133.5	7.5	979	2	Q879Y2

32	133.5	7.5	10578	2	Q81SF5	Q61E55 caenorhabd
33	133.5	7.5	18519	2	Q81SF6	Q81E67 caenorhabd
34	133.5	7.5	18534	2	Q81SF7	Q81E67 caenorhabd
35	133	7.5	722	2	Q26893	Q26893 trypanosoma
36	133	7.5	779	2	Q7YRG3	Q7YRG3 canis famil
37	133	7.5	2032	2	Q7SD73	Q7SD73 neurospora
38	133	7.5	2768	2	Q9VC00	Q9VC00 drosophila
39	132.5	7.5	812	2	Q9AT64	Q9AT64 oryza sativ
40	132	7.4	486	2	Q96RX3	Q96RX3 homo sapien
41	132	7.4	1554	2	Q7RXX1	Q7RXX1 plasmidium
42	131.5	7.4	407	1	IE68_SHV21	Q7RXX1 plasmidium
43	131.5	7.4	2004	2	Q970P7	Q970P7 streptococc
44	131	7.4	459	1	CAH9_HUMAN	Q16790 homo sapien
45	131	7.4	486	2	Q86VQ3	Q86VQ3 homo sapien

ALIGNMENTS

RESULT 1
Q9ALV7 PRELIMINARY; PRT; 348 AA.

AC Q9ALV7; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
DE Acidic repeat protein.
GN Name=arp;
OS Treponema pallidum (subsp. pertenue) (Yaws treponeme).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=168;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC2;
RA Liu H., Steiner B.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342806; AKK01460.2; -
SQ SEQUENCE 348 AA; 37936 MW; E4A446BD82344592 CRC64;

Query Match 100.0%; Score 1776; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 7,9e-100;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MFVRSDMPFKNTAVESINLEKNAKAQAVVIGHAGIPGLLVSLAPAAQAQIGVQAVAV	60
DB	1	MFVRSDMPFKNTAVESINLEKNAKAQAVVIGHAGIPGLLVSLAPAAQAQIGVQAVAV	60
QY	61	RVRTCTGVGGSGTODGLSLASLSRVPARPAQNDPLSSPPAGTVPVRYRTVFFDDR	120
DB	61	RVRTCTGVGGSGTODGLSLASLSRVPARPAQNDPLSSPPAGTVPVRYRTVFFDDR	120
QY	121	LVSPLSREVEDVPKVPSPASEREGEREVEDVPKVPSPASEREGEREVEDVPKVPSPAS	180
DB	121	LVSPLSREVEDVPKVPSPASEREGEREVEDVPKVPSPASEREGEREVEDVPKVPSPAS	180
QY	181	EEGGEREVEDVPKVPSPASEREGEREVEDVPKVPSPASEREGEREVEDVPKVPSPAS	240
DB	181	EEGGEREVEDVPKVPSPASEREGEREVEDVPKVPSPASEREGEREVEDVPKVPSPAS	240
QY	241	PULSSEIVPEEQGRAPVITPEGARGIQPGHYVQIVAFHAIQVOSIVHRYGVEY	300
DB	241	PULSSEIVPEEQGRAPVITPEGARGIQPGHYVQIVAFHAIQVOSIVHRYGVEY	300
QY	301	PLAVEODIHGKVRFTVCVPGQDERGAVLENFORFGKAFLLKKAR	348
DB	301	PLAVEODIHGKVRFTVCVPGQDERGAVLENFORFGKAFLLKKAR	348

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:24:23 ; Search time 104.3 Seconds
(without alignments)
77.871 Million cell updates/sec

Title: US-10-017-168-10

Sequence: 1 PKNTAVEISNLEKNAQAQAVV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : A_Geneseq_16Dec04:*
1: geneeqp19808:*
2: geneeqp19908:*
3: geneeqp20008:*
4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038:*
7: geneeqp20038:*
8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	100	100.0	21	4	AA048322 T. pallid
2	100	100.0	232	4	AA048317 T. pallid
3	100	100.0	312	4	AA048318 T. pallid
4	100	100.0	432	4	AA048316 T. pallid
5	48	48.0	924	5	AB054116 Lactococc
6	48	48.0	924	5	AB054116 Lactococc
7	47	47.0	559	6	AB050839 S. pneumo
8	47	47.0	559	6	AB050839 S. pneumo
9	47	47.0	559	6	AB050839 S. pneumo
10	47	47.0	559	6	AB050839 S. pneumo
11	47	47.0	559	6	AB050839 S. pneumo
12	46	46.0	719	5	AB050839 S. pneumo
13	45	45.0	127	5	AB050839 S. pneumo
14	45	45.0	127	5	AB050839 S. pneumo
15	45	45.0	127	5	AB050839 S. pneumo
16	45	45.0	127	5	AB050839 S. pneumo
17	45	45.0	127	5	AB050839 S. pneumo
18	45	45.0	127	5	AB050839 S. pneumo
19	45	45.0	127	5	AB050839 S. pneumo
20	45	45.0	127	5	AB050839 S. pneumo
21	45	45.0	127	5	AB050839 S. pneumo
22	45	45.0	127	5	AB050839 S. pneumo
23	45	45.0	127	5	AB050839 S. pneumo
24	44	44.0	90	2	AA05260 Amino aci
25	44	44.0	90	2	AA05260 Amino aci

26	44	44.0	100	5	AB04001 Human ORF
27	44	44.0	126	4	AA050260 C glutami
28	44	44.0	223	4	AA052129 Protoninb
29	44	44.0	223	6	AB048648 Protoninb
30	44	44.0	690	5	ADK36997 Novel hum
31	44	44.0	721	4	AA033128 Human pro
32	44	44.0	721	5	AA024543 Human NGV
33	44	44.0	721	5	AA024543 Human NGV
34	44	44.0	721	5	AA024543 Human NGV
35	44	44.0	721	5	AA024543 Human NGV
36	43	43.0	2309	4	AB066232 Human nov
37	42.5	42.5	471	7	AD036078 Human nov
38	42.5	42.5	600	6	AB068187 Photornab
39	42	42.0	96	4	AA014099 Peptide #
40	42	42.0	96	4	AA014099 Peptide #
41	42	42.0	96	4	AA014099 Peptide #
42	42	42.0	96	4	AA014099 Peptide #
43	42	42.0	96	4	AA014099 Peptide #
44	42	42.0	96	4	AA014099 Peptide #
45	42	42.0	96	4	AA014099 Peptide #
46	42	42.0	96	4	AA014099 Peptide #
47	42	42.0	96	4	AA014099 Peptide #
48	42	42.0	96	4	AA014099 Peptide #
49	42	42.0	96	4	AA014099 Peptide #
50	42	42.0	96	4	AA014099 Peptide #
51	42	42.0	96	4	AA014099 Peptide #
52	42	42.0	96	4	AA014099 Peptide #
53	42	42.0	96	4	AA014099 Peptide #
54	42	42.0	96	4	AA014099 Peptide #
55	42	42.0	96	4	AA014099 Peptide #
56	42	42.0	96	4	AA014099 Peptide #
57	41.5	41.5	325	6	AB044241 Protein e
58	41	41.0	66	7	AD06376 Bacterial
59	41	41.0	97	8	AB059866 Bacterial
60	41	41.0	133	7	AD06376 Bacterial
61	41	41.0	133	7	AD06376 Bacterial
62	41	41.0	208	5	AB052220 Bacterial
63	41	41.0	220	5	AB052220 Bacterial
64	41	41.0	236	5	AB051990 Helicobac
65	41	41.0	241	5	AB051990 Helicobac
66	41	41.0	270	5	AB051805 Helicobac
67	41	41.0	283	5	AB051471 Helicobac
68	41	41.0	301	5	AB049115 Helicobac
69	41	41.0	301	5	AB049115 Helicobac
70	41	41.0	301	5	AB049115 Helicobac
71	41	41.0	331	6	AB047212 Protein e
72	41	41.0	331	6	AB047212 Protein e
73	41	41.0	414	6	AB048028 Protein e
74	41	41.0	444	8	AA030821 Human KRP
75	41	41.0	444	8	AA030821 Human KRP
76	41	41.0	444	8	AA030821 Human KRP
77	41	41.0	635	5	ABP73799 Candida a
78	41	41.0	797	5	AB047691 Listeria
79	41	41.0	803	8	AD04865 Bacterial
80	41	41.0	855	4	AB050450 Bacterial
81	41	41.0	907	4	AB053073 Bacterial
82	41	41.0	916	6	AB053073 Bacterial
83	41	41.0	916	6	AB053073 Bacterial
84	41	41.0	916	6	AB053073 Bacterial
85	41	41.0	916	6	AB053073 Bacterial
86	41	41.0	916	6	AB053073 Bacterial
87	41	41.0	916	6	AB053073 Bacterial
88	41	41.0	916	6	AB053073 Bacterial
89	41	41.0	916	6	AB053073 Bacterial
90	41	41.0	916	6	AB053073 Bacterial
91	41	41.0	916	6	AB053073 Bacterial
92	41	41.0	916	6	AB053073 Bacterial
93	41	41.0	916	6	AB053073 Bacterial
94	41	41.0	916	6	AB053073 Bacterial
95	41	41.0	916	6	AB053073 Bacterial
96	41	41.0	916	6	AB053073 Bacterial
97	41	41.0	916	6	AB053073 Bacterial
98	41	41.0	916	6	AB053073 Bacterial

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:40:43 ; Search time 19.95 Seconds
(without alignments)
101.281 Million cell updates/sec

Title: US-10-017-168-10

Perfect score: 100
Sequence: 1 PKNTAVEISNLEKNKAQAVV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_79:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	256	2	F71326	hypothetical prote
2	48.0	924	2	C66725	chromosome segrega
3	47.0	559	2	D95055	PTS system, lactos
4	47.0	559	2	A97925	probable phosphot
5	46.0	719	2	A81358	hypothetical prote
6	45.0	265	2	T35512	hypothetical prote
7	44.5	404	2	F84999	hypothetical prote
8	44.0	244	1	G8BPP4	head size determin
9	44.0	244	2	PA2465	head size determin
10	44.0	778	2	T17679	proline-rich prote
11	44.0	1136	2	F96564	hypothetical prote
12	43.0	554	2	F86244	hypothetical prote
13	43.0	561	2	T49228	plasma membrane H+
14	42.0	115	2	H75491	conserved hypothet
15	42.0	265	2	AC9084	ABC transporter, A
16	42.0	309	2	A42921	transcription elon
17	42.0	369	2	T29207	hypothetical prote
18	42.0	446	2	D90238	aspartokinase (AKH
19	42.0	476	2	D71200	macronuclear alpha
20	42.0	495	2	A41221	internalin protein
21	42.0	673	2	AP1143	hypothetical prote
22	42.0	795	2	T20939	protein-tyrosine-p
23	42.0	1187	1	A53661	pllyl protein homo
24	42.0	1217	2	H82707	hypothetical prote
25	41.0	143	2	G90873	unknown protein en
26	41.0	164	2	D85745	hypothetical prote
27	41.0	228	2	A13082	FlidZ protein (Ad27
28	41.0	228	2	G98203	membrane-bound tet
29	41.0	237	1	S56137	

30	41	41.0	241	2	B97019
31	41	41.0	301	2	AF1257
32	41	41.0	301	2	AB1620
33	41	41.0	326	1	T21924
34	41	41.0	331	1	A30929
35	41	41.0	331	2	F85811
36	41	41.0	331	2	AC0752
37	41	41.0	331	2	F90963
38	41	41.0	331	2	H64957
39	41	41.0	331	2	T27866
40	41	41.0	555	2	F96914
41	41	41.0	619	2	C64696
42	41	41.0	797	2	AH1302
43	41	41.0	797	2	AH1674
44	41	41.0	803	1	E70041
45	41	41.0	1070	2	T30848
46	41	41.0	1188	1	A57064
47	41	41.0	1216	1	A57064
48	41	41.0	1250	2	S60613
49	41	41.0	1250	2	A39578
50	40.5	40.5	2152	2	T45583
51	40.5	40.5	244	2	T22779
52	40.5	40.5	244	2	A75184
53	40.5	40.5	92	2	A11101
54	40.5	40.5	92	2	A11463
55	40.5	40.5	149	2	S51383
56	40.5	40.5	189	2	C64486
57	40.5	40.5	239	2	T02551
58	40.5	40.5	315	2	D70313
59	40.5	40.5	345	2	A96597
60	40.5	40.5	345	2	T41355
61	40.5	40.5	404	2	G85088
62	40.5	40.5	405	2	H71984
63	40.5	40.5	451	2	G82218
64	40.5	40.5	506	2	F86253
65	40.5	40.5	555	2	C95911
66	40.5	40.5	584	2	B82936
67	40.5	40.5	595	2	B97666
68	40.5	40.5	606	1	CX805M
69	40.5	40.5	616	2	C71648
70	40.5	40.5	631	2	H64578
71	40.5	40.5	765	1	JT0383
72	40.5	40.5	767	2	T19690
73	40.5	40.5	808	2	TS1138
74	40.5	40.5	876	2	AB1177
75	40.5	40.5	876	2	AF1534
76	40.5	40.5	1062	2	F83335
77	40.5	40.5	1062	2	T30830
78	40.5	40.5	1287	2	AF2031
79	40.5	40.5	1375	2	T13822
80	40.5	40.5	1526	2	T13823
81	39.5	39.5	156	2	D81343
82	39.5	39.5	345	2	E71843
83	39.5	39.5	49	2	T13184
84	39.5	39.5	68	2	B44993
85	39.5	39.5	117	2	T29913
86	39.5	39.5	128	2	C84873
87	39.5	39.5	128	2	B72230
88	39.5	39.5	180	2	T33142
89	39.5	39.5	212	2	C75093
90	39.5	39.5	243	2	C95313
91	39.5	39.5	243	2	F95288
92	39.5	39.5	253	2	G97267
93	39.5	39.5	259	2	A98098
94	39.5	39.5	259	2	E85943
95	39.5	39.5	259	2	H65071
96	39.5	39.5	292	2	AB2893
97	39.5	39.5	292	2	E97668
98	39.5	39.5	294	2	F87397
99	39.5	39.5	297	2	S17474
100	39.5	39.5	311	2	E82915
101	39.5	39.5	313	2	AD1285
102	39.5	39.5	314	2	H71802

1-acyl-sn-glycerol
GTP binding protei
GTP binding protei
hypothetical prote
flagellar motor sw
hypothetical prote
flagellar motor sw
flagellar motor sw
flagellar motor sw
flagellar motor sw
hypothetical prote
membrane-associate
hypothetical prote
primosomal replica
probable copper-tr
buffy receptor - p
protein-tyrosine-p
SSD1 protein - yea
hypothetical prote
hypothetical prote
ATP-binding transp
B. subtilis YabO p
B. subtilis YabO p
probable membrane
hypothetical prote
probable carboxyme
riboflavin kinase
hypothetical prote
Sut1 homolog - fis
hypothetical prote
probable carboxyme
sensor histidine k
hypothetical prote
probable protein,
conserved hypothet
DNA primase (EC 2.
NADH2 dehydrogenas
DNA primase (EC 2.
conserved hypothet
anthranilate synth
hypothetical prote
probable glutamate
cation transportin
cation transportin
RND multidrug effl
hypothetical prote
two-component hybr
frazzled gene prot
frazzled gene prot
oxygen-independent
hypothetical prote
flagellar repetiti
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
cytochrome-c oxida
probable GntR-type
PHP superfamily hy
hypothetical prote
hypothetical prote
metal dependant be
hypothetical prote
dihydrodipicolinat
hypothetical prote
ribosomal protein
glycerate dehydrog
probable outer mem

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:25:43 ; Search time 98.35 Seconds
(without alignments)
109.341 Million cell updates/sec

Title: US-10-017-168-10

Perfect score: 100

Sequence: 1 PKMTAVEISNLEKNKAQAVV 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database: Uniprot_03:*

1: uniprot_prot:*

SUMMARIES

Result No. Score Match Length DB ID Description

1	100	100.0	256	2	083448	083448 treponema p
2	100	100.0	348	2	09ALV7	09ALV7 treponema p
3	100	100.0	393	2	093CA3	093CA3 treponema p
4	100	100.0	428	2	08ALV6	08ALV6 treponema p
5	100	100.0	432	2	051953	051953 treponema p
6	100	100.0	548	2	093CA4	093CA4 treponema p
7	76	76.0	458	2	073NG7	073NG7 treponema d
8	51	51.0	602	2	07NKL4	07NKL4 gloeobacter
9	50	50.0	266	2	07UPY9	07UPY9 rhodopirell
10	48	48.0	293	2	08DT43	08DT43 streptococc
11	48	48.0	924	2	09CHC9	09CHC9 lactococcu
12	48	48.0	1174	2	0932X6	0932X6 lactococcu
13	48	48.0	1174	2	07BBS2	07BBS2 lactococcu
14	47.5	47.5	282	1	06BML8	06BML8 debarymyce
15	47	47.0	126	1	Y334_BUCBP	Y334_BUCBP
16	47	47.0	559	2	097SA8	097SA8 streptococc
17	47	47.0	559	2	097SA8	097SA8 streptococc
18	47	47.0	559	2	08DQZ0	08DQZ0 streptococc
19	46	46.0	719	2	09P74	09P74 campylobact
20	46	46.0	846	2	07R6S2	07R6S2 giardia lam
21	45	45.0	253	2	08ED43	08ED43 shewanella
22	45	45.0	265	2	09X7Y9	09X7Y9 streptomyce
23	45	45.0	321	1	08NCT0	08NCT0 homo sapien
24	45	45.0	325	2	06QPK1	06QPK1 lycopersico
25	45	45.0	447	2	06QPK1	06QPK1 lycopersico
26	45	45.0	587	2	07P209	07P209 fusobacteri
27	45	45.0	1192	2	0869E1	0869E1 dictyosteli
28	44.5	44.5	404	1	ISCS_BUCAI	ISCS_BUCAI
29	44.5	44.5	126	2	08NT52	08NT52 corynebacte
30	44	44.0	126	2	08XLM9	08XLM9 clostridium
31	44	44.0	126	2	08XLM9	08XLM9 clostridium

32	44	44.0	241	2	Q6MAX8	Q6MAX8 parachlamy
33	44	44.0	244	1	VSID_BBP4	VSID_BBP4
34	44	44.0	244	2	Q7M2A2	Q7M2A2 bacterioph
35	44	44.0	256	2	Q7ORN9	Q7ORN9 giardia lam
36	44	44.0	721	1	BBS2_HUMAN	BBS2_HUMAN
37	44	44.0	835	2	Q7RN80	Q7RN80
38	44	44.0	1336	2	Q9SSP7	Q9SSP7
39	44	44.0	1259	2	Q7S528	Q7S528
40	44	44.0	1299	2	Q84509	Q84509
41	44	44.0	1464	2	Q871F7	Q871F7
42	44	44.0	1686	2	Q8IFP9	Q8IFP9
43	43.5	43.5	201	1	HAW1_RALSO	HAW1_RALSO
44	43	43.0	130	1	Y142_LEUMC	Y142_LEUMC
45	43	43.0	148	2	Q74FE1	Q74FE1
46	43	43.0	184	2	Q97W5	Q97W5
47	43	43.0	184	2	Q97W5	Q97W5
48	43	43.0	292	2	Q9HK60	Q9HK60
49	43	43.0	304	2	Q6FIV2	Q6FIV2
50	43	43.0	423	2	Q6HJ6	Q6HJ6
51	43	43.0	554	2	Q23691	Q23691
52	43	43.0	670	2	Q6HJ6	Q6HJ6
53	43	43.0	973	2	Q81L59	Q81L59
54	43	43.0	1515	2	Q9LHR7	Q9LHR7
55	43	43.0	1609	2	Q7RHX7	Q7RHX7
56	43	43.0	2310	2	Q9W2U7	Q9W2U7
57	42.5	42.5	586	2	Q7N1J2	Q7N1J2
58	42	42.0	115	2	Q9RMK4	Q9RMK4
59	42	42.0	129	2	Q6AM18	Q6AM18
60	42	42.0	201	2	Q6NV24	Q6NV24
61	42	42.0	254	2	Q8TOM6	Q8TOM6
62	42	42.0	254	2	Q9VSM4	Q9VSM4
63	42	42.0	265	2	Q8YUW1	Q8YUW1
64	42	42.0	300	2	Q8EPY0	Q8EPY0
65	42	42.0	309	1	TPS2_YEAST	TPS2_YEAST
66	42	42.0	321	2	Q7R8K6	Q7R8K6
67	42	42.0	369	1	YOK3_CABEL	YOK3_CABEL
68	42	42.0	446	2	Q97ZL7	Q97ZL7
69	42	42.0	476	2	Q59547	Q59547
70	42	42.0	476	2	Q7NM21	Q7NM21
71	42	42.0	478	2	Q7VJ10	Q7VJ10
72	42	42.0	492	2	Q6BXNO	Q6BXNO
73	42	42.0	495	1	TEBA_OXYNO	TEBA_OXYNO
74	42	42.0	497	2	Q81503	Q81503
75	42	42.0	504	2	Q7QRL8	Q7QRL8
76	42	42.0	519	2	Q6IG01	Q6IG01
77	42	42.0	548	2	Q6EP13	Q6EP13
78	42	42.0	549	2	Q6W270	Q6W270
79	42	42.0	673	2	Q8Y9H9	Q8Y9H9
80	42	42.0	682	2	Q6FV57	Q6FV57
81	42	42.0	686	2	Q6TWX9	Q6TWX9
82	42	42.0	702	2	Q7RPO8	Q7RPO8
83	42	42.0	715	1	BBS2_BRARE	BBS2_BRARE
84	42	42.0	715	2	Q6D145	Q6D145
85	42	42.0	715	2	Q6PCAO	Q6PCAO
86	42	42.0	723	2	Q6LYZ8	Q6LYZ8
87	42	42.0	796	2	Q8R7F1	Q8R7F1
88	42	42.0	819	2	Q22063	Q22063
89	42	42.0	854	2	Q7MD06	Q7MD06
90	42	42.0	854	2	Q8D6U5	Q8D6U5
91	42	42.0	952	2	Q6FPO4	Q6FPO4
92	42	42.0	1087	2	Q6NSK5	Q6NSK5
93	42	42.0	1105	2	Q6NU19	Q6NU19
94	42	42.0	1125	2	Q9NQW6	Q9NQW6
95	42	42.0	1130	2	Q9XZC1	Q9XZC1
96	42	42.0	1187	2	Q28613	Q28613
97	42	42.0	1217	2	Q9PB04	Q9PB04
98	42	42.0	1292	2	Q757G8	Q757G8
99	42	42.0	1496	2	Q6BMD2	Q6BMD2
100	41.5	41.5	195	2	Q7VDL6	Q7VDL6
101	41.5	41.5	325	2	Q8DS06	Q8DS06
102	41.5	41.5	644	2	Q81IV7	Q81IV7
103	41	41.0	101	2	Q7UJZ8	Q7UJZ8
104	41	41.0	143	2	Q7AECS	Q7AECS

Q6MAX8 parachlamy
P05461 bacterioph
Q7M2A2 bacterioph
Q7QRL8 giardia lam
Q9XCV9 homo sapien
Q7RN80 plasmodium
Q9SAP7 arbidopais
Q6S28 neurospora
Q64509 parametium
Q61F7 neurospora
Q61F9 plasmodium
Q6XCF4 ralteonria s
P57117 leucostococ
Q74FE1 geobacter s
Q57W5 acidianus t
Q5HK60 thermoplas
Q6FIV2 mesoplasma
Q23691 dictyosteli
Q6HJ6 debarymyce
Q9LYJ2 arbidopais
Q81H8 plasmodium
Q9LH7 arbidopais
Q7RHX7 plasmodium
Q9W2U7 drosophila
Q7N1J2 photorhabd
Q9W44 deinococcus
Q6AM18 desulfotale
Q6NV24 brachydantio
Q8TOM6 drosophila
Q9VSM4 drosophila
Q8YUW1 anabena sp
Q8EPY0 oceanobacil
P77273 saccharomyc
Q7R9K6 plasmodium
P91478 caenorhabd
Q97ZL7 sulfolobus
Q59547 pyrococcus
Q7N41 chromobacte
Q7VJ10 prochloroc
Q5BXNO debarymyce
P29549 oxytricha n
Q31503 plasmodium
Q7QRL8 giardia lam
Q5IG01 rattus norv
Q6EP13 candida gla
Q6W270 rhizobium s
Q8Y9H9 listeria mo
Q6FV57 candida gla
Q6TWX9 schistosoma
Q7RPO8 plasmodium
Q9SAP7 brachydantio
Q6D145 brachydantio
Q6PCAO brachydantio
Q6LYZ8 methanococ
Q8R7F1 thermoaer
Q22063 caenorhabd
Q7MD06 vibrio vuln
Q8D6U5 vibrio vuln
Q6FPO4 candida gla
Q6NSK5 homo sapien
Q6NU19 homo sapien
Q9NQW6 xenopus lae
Q9XZC1 boophilus m
Q28613 oxytricha s
Q9PB04 xyloella fas
Q757G8 ashbya gos
Q6BMD2 debarymyce
Q7VDL6 prochloroc
Q8DS06 streptococ
Q81IV7 plasmodium
Q7UJZ8 rhodopirell
Q7AECS escherichia

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:24:23 ; Search time 94.3667 Seconds

(without alignments)
77.871 Million cell updates/sec

Title: US-10-017-168-7

Perfect score: 92

Sequence: 1 LVSPUREVEDAPKVEFPAS 19

Scoring table: BLOSUM62

Searched: 2105692 seqs, 366760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :
1: Genesepq16Dec04:*
2: Genesepq19908:*
3: Genesepq20008:*
4: Genesepq20018:*
5: Genesepq20028:*
6: Genesepq20038:*
7: Genesepq20038:*
8: Genesepq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	19	4	AAU43202
2	81.5	88.6	432	4	AAU43202
3	77.5	84.2	232	4	AAU43202
4	77.5	84.2	312	4	AAU43202
5	69	75.0	20	4	AAU43202
6	64	69.6	20	4	AAU43202
7	60	65.2	20	4	AAU43202
8	55	59.8	20	4	AAU43202
9	53	57.6	20	4	AAU43202
10	47	51.1	299	4	AAU43202
11	47	51.1	299	4	AAU43202
12	45	48.9	131	8	ADQ53613
13	45	48.9	197	4	AAU43202
14	45	48.9	198	4	AAU43202
15	45	48.9	198	4	AAU43202
16	45	48.9	198	4	AAU43202
17	45	48.9	198	4	AAU43202
18	44	46.7	463	2	AAU43202
19	43	46.7	463	2	AAU43202
20	43	46.7	463	2	AAU43202
21	43	46.7	463	2	AAU43202
22	43	46.7	463	2	AAU43202
23	43	46.7	463	2	AAU43202
24	43	46.7	463	2	AAU43202
25	43	46.7	463	2	AAU43202

26	42.5	46.2	137	4	AAU43202
27	42.5	46.2	137	6	AAU43202
28	42.5	46.2	425	4	AAU43202
29	42.5	46.2	425	6	AAU43202
30	42.5	46.2	481	6	AAU43202
31	42	45.7	51	6	AAU43202
32	42	45.7	51	6	AAU43202
33	42	45.7	103	7	ADP59039
34	42	45.7	160	5	ADP59039
35	42	45.7	160	5	ADP59039
36	42	45.7	198	8	ADP59039
37	42	45.7	254	8	ADP59039
38	42	45.7	503	2	AAU43202
39	42	45.7	557	2	AAU43202
40	42	45.7	783	8	ADP59039
41	42	45.7	783	8	ADP59039
42	42	45.7	783	8	ADP59039
43	42	45.7	783	8	ADP59039
44	42	45.7	783	8	ADP59039
45	42	45.7	783	8	ADP59039
46	42	45.7	783	8	ADP59039
47	42	45.7	783	8	ADP59039
48	42	45.7	783	8	ADP59039
49	42	45.7	783	8	ADP59039
50	42	45.7	783	8	ADP59039
51	42	45.7	783	8	ADP59039
52	42	45.7	783	8	ADP59039
53	42	45.7	783	8	ADP59039
54	42	45.7	783	8	ADP59039
55	42	45.7	783	8	ADP59039
56	42	45.7	783	8	ADP59039
57	42	45.7	783	8	ADP59039
58	42	45.7	783	8	ADP59039
59	42	45.7	783	8	ADP59039
60	42	45.7	783	8	ADP59039
61	42	45.7	783	8	ADP59039
62	42	45.7	783	8	ADP59039
63	42	45.7	783	8	ADP59039
64	42	45.7	783	8	ADP59039
65	42	45.7	783	8	ADP59039
66	42	45.7	783	8	ADP59039
67	42	45.7	783	8	ADP59039
68	42	45.7	783	8	ADP59039
69	42	45.7	783	8	ADP59039
70	42	45.7	783	8	ADP59039
71	42	45.7	783	8	ADP59039
72	42	45.7	783	8	ADP59039
73	42	45.7	783	8	ADP59039
74	42	45.7	783	8	ADP59039
75	42	45.7	783	8	ADP59039
76	42	45.7	783	8	ADP59039
77	42	45.7	783	8	ADP59039
78	42	45.7	783	8	ADP59039
79	42	45.7	783	8	ADP59039
80	42	45.7	783	8	ADP59039
81	42	45.7	783	8	ADP59039
82	42	45.7	783	8	ADP59039
83	42	45.7	783	8	ADP59039
84	42	45.7	783	8	ADP59039
85	42	45.7	783	8	ADP59039
86	42	45.7	783	8	ADP59039
87	42	45.7	783	8	ADP59039
88	42	45.7	783	8	ADP59039
89	42	45.7	783	8	ADP59039
90	42	45.7	783	8	ADP59039
91	42	45.7	783	8	ADP59039
92	42	45.7	783	8	ADP59039
93	42	45.7	783	8	ADP59039
94	42	45.7	783	8	ADP59039
95	42	45.7	783	8	ADP59039
96	42	45.7	783	8	ADP59039
97	42	45.7	783	8	ADP59039
98	42	45.7	783	8	ADP59039
99	42	45.7	783	8	ADP59039
100	42	45.7	783	8	ADP59039

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M protein - protein search, using sw model

Run on: April 28, 2005, 17:25:43 ; Search time 88.9833 Seconds
(without alignments)

109.341 Million cell updates/sec

Title: US-10-017-168-7

Effective score: 92
Sequence: 1 LVSPUREVDADPKVPEPAS 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 500 summaries

Database : Uniprot_03:*

1: uniprot_03:prot:*
2: uniprot_03:trmb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	81.5	88.6	256	2	083448	083448 tleponema p
2	81.5	88.6	432	2	051953	051953 tleponema p
3	81.5	88.6	548	2	093CA4	093CA4 tleponema p
4	77.5	84.2	348	2	09ALV7	09ALV7 tleponema p
5	77.5	84.2	428	2	09ALV6	09ALV6 tleponema p
6	75	81.5	393	2	093CA3	093CA3 tleponema p
7	58	63.0	227	2	083449	083449 tleponema p
8	53	57.6	258	2	06N162	06N162 tleponema p
9	49	53.3	167	2	052680	052680 tleponema p
10	49	53.3	380	2	09AVT0	09AVT0 tleponema p
11	48	52.2	368	2	070784	070784 picea abies
12	47	51.1	299	1	YEGS_ECOLI	YEGS_ECOLI
13	47	51.1	299	2	083V54	083V54 escherichia
14	47	51.1	299	2	07UCB0	07UCB0 shigella fl
15	47	51.1	299	2	083K10	083K10 shigella fl
16	47	51.1	299	2	08PFZ2	08PFZ2 escherichia
17	47	51.1	299	2	08X7H7	08X7H7 escherichia
18	47	51.1	761	2	09D9U3	09D9U3 mus musculus
19	47	51.1	778	2	06PC00	06PC00 mus musculus
20	47	51.1	792	2	069XV8	069XV8 oryza sativ
21	47	51.1	1040	2	070G14	070G14 anopheles g
22	46	50.0	195	1	TATB_XANCP	TATB_XANCP
23	46	50.0	434	2	093X74	093X74 xanthomonas
24	46	50.0	434	2	075U06	075U06 brassica ra
25	46	50.0	2192	2	081BW7	081BW7 plasmodium
26	45	48.9	101	2	09ERH9	09ERH9 cavia porce
27	45	48.9	137	2	06AHX3	06AHX3 homo sapien
28	45	48.9	142	2	08TER0	08TER0 homo sapien
29	45	48.9	194	2	09YF07	09YF07 aetopyrum p
30	45	48.9	198	1	DUC5_BOVIN	DUC5_BOVIN
31	45	48.9	198	1	DUC5_HUMAN	DUC5_HUMAN

32	45	48.9	198	1	DUC5_MOUSE	P60904 mus musculus
33	45	48.9	198	1	DUC5_RAT	P60905 rattus norv
34	45	48.9	204	2	0921J3	0921J3 mus musculus
35	45	48.9	390	2	081HV9	081HV9 bacillus ce
36	45	48.9	426	2	08MU99	08MU99 bacillus ce
37	45	48.9	497	2	08MPR7	08MPR7 trypanosoma
38	45	48.9	542	2	023446	023446 caenorhabdi
39	45	48.9	612	2	096019	096019 drosophila
40	45	48.9	612	2	09YGA5	09YGA5 drosophila
41	45	48.9	662	1	GLCX_YERPE	GLCX_YERPE
42	45	48.9	662	2	0664T3	0664T3
43	45	48.9	1135	2	09YHD3	09YHD3
44	45	48.9	1247	2	0805Z8	0805Z8 ceratopithe
45	45	47.8	149	2	069XH7	069XH7 oryza sativ
46	44	47.8	274	2	028716	028716 archaeoglob
47	44	47.8	302	2	06D9E8	06D9E8 errinita car
48	44	47.8	326	2	062F80	062F80 burkholderi
49	44	47.8	326	2	063XN0	063XN0 burkholderi
50	44	47.8	326	2	092109	092109 mus musculu
51	44	47.8	763	2	07R1Q1	07R1Q1 giardia lam
52	44	47.8	763	2	092239	092239 mus musculu
53	44	47.8	809	2	0657N5	0657N5 mus musculu
54	44	47.8	813	2	08C9X6	08C9X6 oryza sativ
55	44	47.8	899	2	08KJ56	08KJ56 mus musculu
56	44	47.8	1025	2	089000	089000 rattus norv
57	43.5	47.3	193	1	NOIC_SYNY3	NOIC_SYNY3
58	43.5	47.3	651	2	061L49	061L49
59	43	46.7	230	1	PYRF_HAEIN	PYRF_HAEIN
60	43	46.7	403	1	ASSY_BACSU	ASSY_BACSU
61	43	46.7	404	2	098GM2	098GM2 haemophilus
62	43	46.7	434	1	MDA3_ARATH	MDA3_ARATH
63	43	46.7	434	1	081N45	081N45 mesembryant
64	43	46.7	477	2	093YG1	093YG1
65	43	46.7	513	2	0948P8	0948P8
66	43	46.7	672	2	070199	070199
67	43	46.7	792	2	08CPY0	08CPY0
68	43	46.7	1091	2	088LM4	088LM4 pseudomonas
69	43	46.7	4293	2	008852	008852 mus musculu
70	42.5	46.2	682	2	06A822	06A822 propionibac
71	42.5	46.2	785	1	METE_DESVH	METE_DESVH
72	42	45.7	114	2	0567E1	0567E1 desulfovibrio
73	42	45.7	139	1	YS87_MYCTU	YS87_MYCTU
74	42	45.7	139	1	YT11_MYCBO	YT11_MYCBO
75	42	45.7	192	2	094GC9	094GC9 mycobacteri
76	42	45.7	198	1	SCPB_LISMO	SCPB_LISMO
77	42	45.7	198	1	071Y64	071Y64 listeria mo
78	42	45.7	208	1	CP23_CHICK	CP23_CHICK
79	42	45.7	208	1	07Y5U0	07Y5U0
80	42	45.7	224	2	0715F2	0715F2
81	42	45.7	243	2	0806C8	0806C8 ceratopithe
82	42	45.7	244	2	0821E4	0821E4 chlamydomoph
83	42	45.7	244	2	08JHB7	08JHB7 gallus gall
84	42	45.7	255	2	065JF0	065JF0 gallus gall
85	42	45.7	255	2	098601	098601 bacillus li
86	42	45.7	299	2	08UCR8	08UCR8 rhizobium i
87	42	45.7	404	2	09X6W3	09X6W3 agrobacteri
88	42	45.7	405	2	092VDP9	092VDP9 rhizobium m
89	42	45.7	405	2	07CWP7	07CWP7 agrobacteri
90	42	45.7	417	2	09HGG5	09HGG5 mucor indic
91	42	45.7	460	2	09HKK1	09HKK1 thermoplasma
92	42	45.7	460	2	06G0P1	06G0P1 brachydanio
93	42	45.7	482	2	0721V4	0721V4 thermus the
94	42	45.7	505	2	07V5B3	07V5B3 prochlorococ
95	42	45.7	506	1	ER11_BRANA	ER11_BRANA
96	42	45.7	575	2	072J64	072J64 thermus the
97	42	45.7	582	2	06AX30	06AX30 brachydanio
98	42	45.7	626	2	090ZT2	090ZT2 brachydanio
99	42	45.7	646	2	09CA83	09CA83 arabidopsis
100	42	45.7	663	2	09WA03	09WA03 arabidopsis
101	42	45.7	669	2	089BR3	089BR3 brachydanio
102	42	45.7	768	2	08SRC6	08SRC6 encephalito
103	42	45.7	873	2	08RTT3	08RTT3 uncultured
104	42	45.7	873	2	06SFD0	06SFD0 uncultured

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:40:43 ; Search time 18.05 Seconds

(without alignment)
101.281 Million cell updates/sec

Title: US-10-017-168-7

Perfect score: 92

Sequence: 1 LVSPLREVEDAPKXVEPAS 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

PIR_79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81.5	88.6	256	2	F71326
2	58	63.0	227	2	G71326
3	49	53.3	167	2	S52220
4	47	51.1	299	2	F85835
5	47	51.1	299	2	D90990
6	47	51.1	299	2	E64975
7	45	48.9	194	2	F72775
8	45	48.9	198	2	S70515
9	45	48.9	198	2	I52655
10	45	48.9	542	2	T29707
11	45	48.9	662	2	AG0479
12	45	48.9	1135	2	T30561
13	44	47.8	274	2	C69444
14	44	47.8	624	2	T27096
15	43.5	47.3	193	2	FEYB01
16	43	46.7	230	2	BE4111
17	43	46.7	403	2	B69589
18	43	46.7	434	2	T47545
19	42	45.7	139	2	B70925
20	42	45.7	198	2	AF1318
21	42	45.7	209	2	A36344
22	42	45.7	402	2	AE2894
23	42	45.7	404	2	H95937
24	42	45.7	404	2	T44600
25	42	45.7	405	2	H97669
26	42	45.7	506	2	T07942
27	42	45.7	646	2	E86828
28	41.5	45.1	137	2	B71136
29	41.5	45.1	566	1	NIPSRP

30	41.5	45.1	591	2	B54354	calnexin precursor
31	41.5	45.1	591	2	CE4354	calnexin precursor
32	41	44.6	210	2	S41631	hypoxanthine phosph
33	41	44.6	217	2	G75219	hypothetical prote
34	41	44.6	224	2	F69601	hypothetical prote
35	41	44.6	243	2	E81652	cytidylate kinase
36	41	44.6	355	2	S11152	conserved hypotet
37	41	44.6	355	2	F98084	oligopeptide trans
38	41	44.6	355	2	F95220	hypothetical prote
39	41	44.6	355	2	F95220	hypothetical prote
40	41	44.6	404	2	D85642	hypothetical prote
41	41	44.6	404	2	G90781	hypothetical prote
42	41	44.6	428	2	T32952	hypothetical prote
43	41	44.6	498	2	PC6300	hypothetical prote
44	41	44.6	510	2	G72464	synaptochrome X -
45	41	44.6	572	2	S58889	hypothetical prote
46	41	44.6	572	2	JC5317	collapsin response
47	41	44.6	572	2	S49985	dihydropyrimidinas
48	41	44.6	648	2	T20144	hypothetical prote
49	41	44.6	662	2	B72114	hypothetical prote
50	41	44.6	662	2	E86509	hypothetical prote
51	41	44.6	886	2	H69378	synaptochrome X -
52	41	44.6	897	2	F71816	hypothetical prote
53	41	44.6	971	2	D70128	collapsin response
54	41	44.6	1151	2	T24541	dihydropyrimidinas
55	41	44.6	2717	2	A34203	hypothetical prote
56	41	44.6	3759	2	A35085	RNA ligase Cp0624
57	40.5	44.0	3828	2	T13857	DNA ligase (import
58	40.5	44.0	439	2	T16414	conserved hypotet
59	40.5	44.0	1330	2	H89567	conserved hypotet
60	40.5	44.0	2186	2	T24194	DNA-binding protei
61	40	43.5	217	2	B71203	lithorax protein
62	40	43.5	255	2	G69319	lithorax protein
63	40	43.5	306	2	F70603	hypothetical prote
64	40	43.5	325	2	S58146	hypothetical prote
65	40	43.5	357	2	A33950	conserved hypotet
66	40	43.5	399	2	JC4215	hypothetical prote
67	40	43.5	409	2	T43599	YopM protein - Yer
68	40	43.5	438	2	D70528	T-cell reactive pr
69	40	43.5	467	2	AH3437	yop targeted effec
70	40	43.5	624	2	PC6003	hypothetical prote
71	40	43.5	732	1	S73715	DNA repair protein
72	40	43.5	743	2	G83726	surface membrane p
73	40	43.5	747	1	TNBR82	cytolactone acces
74	40	43.5	1146	2	S07915	assilatory nitra
75	40	43.5	1146	2	A48206	82.3K alpha trans
76	40	43.5	1405	2	T27969	RF2 protein - Yeas
77	39.5	42.9	203	2	A12385	calcium-activated
78	39.5	42.9	356	2	A41664	hypothetical prote
79	39.5	42.9	589	2	D89997	peroxiredoxin (imp
80	39.5	42.9	582	2	A46673	calnexin - human
81	39.5	42.9	592	2	I53260	calnexin precursor
82	39.5	42.9	593	1	A37273	calnexin - human
83	39.5	42.9	809	2	T11695	calnexin precursor
84	39	42.4	56	2	E83079	phospholipase D (E
85	39	42.4	132	2	AH2584	hypothetical prote
86	39	42.4	132	2	G97366	hypothetical prote
87	39	42.4	231	2	H64466	ndrd protein (limp
88	39	42.4	246	2	H72497	hypothetical prote
89	39	42.4	263	2	C70741	probable NH(3)-dep
90	39	42.4	267	2	E72538	hypothetical prote
91	39	42.4	281	1	S34626	probable HRSa prot
92	39	42.4	284	2	H87524	translation elonga
93	39	42.4	315	2	B99607	hypothetical prote
94	39	42.4	317	2	AF1184	hypothetical prote
95	39	42.4	369	2	A39157	oxidoeductases ho
96	39	42.4	369	2	A39157	oxidoeductases ho
97	39	42.4	374	2	AE2337	probable RNA helic
98	39	42.4	393	2	JEO180	hypothetical prote
99	39	42.4	433	2	T06407	phosphopentomutase
100	39	42.4	433	2	A55333	monodehydroascorba
101	39	42.4	434	2	JU0182	monodehydroascorba
102	39	42.4	439	2	E97079	sugar-binding peri

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:24:23 ; Search time 99.3333 Seconds
(without alignments)
77.871 Million cell updates/sec

Title: US-10-017-168-8

Perfect score: 100

Sequence: 1 SREVEDAPKVEVPASEREKG 20

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying Chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp19808.*
2: Geneseqp19808.*
3: Geneseqp20008.*
4: Geneseqp20008.*
5: Geneseqp20008.*
6: Geneseqp20008.*
7: Geneseqp20008.*
8: Geneseqp20008.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	20	4	AAB48320 T. pallid
2	100	100.0	432	4	AAB48316 T. pallid
3	96	96.0	232	4	AAB48317 T. pallid
4	96	96.0	312	4	AAB48318 T. pallid
5	91	91.0	20	4	AAB48329 T. pallid
6	87	87.0	20	4	AAB48327 T. pallid
7	82	82.0	20	4	AAB48328 T. pallid
8	69	69.0	19	4	AAB48319 T. pallid
9	68	68.0	20	4	AAB48330 T. pallid
10	67	67.0	20	4	AAB48321 T. pallid
11	55	55.0	21	4	AAB48325 T. pallid
12	51	51.0	434	3	AAG38717 Arabidops
13	51	51.0	434	3	AAG38717 Arabidops
14	51	51.0	434	3	AAG38717 Arabidops
15	49	49.0	113	5	ABP03876 Human ORF
16	49	49.0	541	4	AAU54787 Human ORF
17	49	49.0	541	4	ABM51306 Propionib
18	49	49.0	541	4	ABM51306 Propionib
19	48	48.0	296	6	ABM51306 Propionib
20	47	47.0	38	5	ABP08658 Human ORF
21	46	46.0	612	4	ABM71474 Drosophi
22	46	46.0	197	4	AAW80072 Human pro
23	46	46.0	198	6	ABR57259 Human cys
24	46	46.0	198	6	ABR57259 Human cys
25	46	46.0	198	8	ABM82286 Tumour-as

26	46	46.0	261	8	ADJ76332	AdJ76332 Marker ge
27	46	46.0	464	7	ABO77466	AbO77466 Pseudomon
28	46	46.0	1326	3	AAAG4239	AAg42239 Arabidops
29	46	46.0	1321	3	AAAG4238	AAg42238 Arabidops
30	46	46.0	1351	3	AAAG4237	AAg42237 Arabidops
31	45	45.0	161	3	AAAG25917	AAg25917 Zea mays
32	45	45.0	170	6	ADAS5215	AdAS5215 Human pro
33	45	45.0	265	4	AAAB80279	AAb80279 Human pro
34	45	45.0	266	4	AAAB64379	AAb64379 Human pro
35	45	45.0	266	4	AAAB39738	AAb39738 Human pol
36	45	45.0	271	7	AAEM85531	AAm85531 Human pro
37	45	45.0	277	4	AAAB80305	AAb80305 Human pro
38	45	45.0	277	4	AAAB80347	AAb80347 Human pro
39	45	45.0	288	4	AAAB80343	AAb80343 Human pro
40	45	45.0	289	4	AAAM41524	AAm41524 Human pro
41	45	45.0	304	3	AAAB57037	AAb57037 Human pro
42	45	45.0	519	6	ABU20235	ABu20235 Murine BH
43	45	45.0	579	8	AAO24552	AAo24552 Murine BH
44	45	45.0	944	4	ABBB60979	ABb60979 Drosophi
45	44.5	44.5	108	4	AAAM5886	AAm5886 Peptide #
46	44.5	44.5	108	4	ABM34874	ABm34874 Peptide #
47	44.5	44.5	108	4	AAAB28394	AAb28394 Peptide #
48	44.5	44.5	108	4	ABBB29700	ABb29700 Peptide #
49	44.5	44.5	108	4	ABBB20291	ABb20291 Peptide #
50	44.5	44.5	108	4	AAAM68062	AAm68062 Human bon
51	44.5	44.5	108	4	AAAM55684	AAm55684 Human bra
52	44.5	44.5	108	4	ABGA9712	ABg49712 Human liv
53	44.5	44.5	108	4	AAAG3621	AAg3621 Peptide #
54	44.5	44.5	108	4	ABGG37588	ABg37588 Human pep
55	44.5	44.5	235	5	AD116506	Ad116506 Human NOV
56	44.5	44.5	235	8	ADN42160	ADn42160 Human NOV
57	44.5	44.5	247	5	AD116502	Ad116502 Human NOV
58	44.5	44.5	247	5	AD116500	Ad116500 Human NOV
59	44.5	44.5	247	5	AD116504	Ad116504 Human NOV
60	44.5	44.5	247	6	ADAI10977	ADa10977 Human NOV
61	44.5	44.5	247	8	ADN42154	ADn42154 Human NOV
62	44.5	44.5	247	8	ADN42156	ADn42156 Human NOV
63	44.5	44.5	247	8	ADN42158	ADn42158 Human NOV
64	44.5	44.5	253	5	AD116788	Ad116788 Human NOV
65	44.5	44.5	253	8	ADN42442	ADn42442 Human NOV
66	44.5	44.5	267	5	AD116813	Ad116813 Human NOV
67	44.5	44.5	280	3	AAAB56833	AAb56833 Human pro
68	44.5	44.5	297	5	ABBS5067	ABb55067 Lactococc
69	44.5	44.5	306	7	ADBB80338	ADb80338 Human MDD
70	44.5	44.5	468	8	ADBO9637	ADb09637 Human pro
71	44.5	44.5	727	5	AD116812	Ad116812 Human NOV
72	44.5	44.5	772	5	AD116811	Ad116811 Human NOV
73	44.5	44.5	792	4	AAAG82199	AAg82199 S. epider
74	44.5	44.5	801	5	ABPA40739	ABp40739 Stephyloc
75	44.5	44.5	801	8	ADSO8045	ADs08045 Stephyloc
76	44.5	44.5	964	7	ADBB4183	ADb4183 Human pro
77	44.5	44.5	1106	7	ADMO5616	ADm05616 Human pro
78	44	44.0	86	7	ADCC31468	ADc31468 Human nov
79	44	44.0	214	4	ABGC04974	ABg04974 Novel hum
80	44	44.0	266	3	AAAB58897	AAb58897 Breast an
81	44	44.0	297	5	AAAB7878	AAb7878 M. tuberc
82	44	44.0	297	5	ABG30907	ABg30907 Mycobacte
83	44	44.0	410	4	AAAM38850	AAm38850 Human pol
84	44	44.0	440	4	AAAM40636	AAm40636 Human pol
85	44	44.0	440	8	ADMB7682	ADm7682 Human EST
86	44	44.0	525	5	ABPA1870	ABp1870 Human ova
87	44	44.0	525	4	AAAB70622	AAb70622 Human GLI
88	44	44.0	528	7	AAAB70621	AAb70621 Human GLI
89	44	44.0	528	7	ADPF9128	ADf69128 Human MP5
90	44	44.0	528	8	ADMB7224	ADm7224 Human pro
91	44	44.0	556	6	ABBU11480	ABu11480 Human MDD
92	44	44.0	606	6	ABBS88889	ABb88889 Drosophi
93	44	44.0	754	7	ADBB6201	ADb6201 Klebsiell
94	44	44.0	754	7	ADBB6201	ADb6201 Klebsiell
95	44	44.0	1046	5	AAOI7712	AAo77112 Human GII
96	44	44.0	1106	4	AAAB06644	AAb06644 Human CUB
97	44	44.0	1106	4	AAAB70611	AAb70611 Human GLI
98	44	44.0	1106	5	AAU12085	AAu12085 Human gII

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:40:43 ; Search time 19 Seconds
(without alignments)
101.281 Million cell updates/sec

Title: US-10-017-168-8
Perfect score: 100
Sequence: 1 SREVEDAPKVEPASEREGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database:
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	256	2 F71326	hypothetical prote
2	73	73.0	227	2 G71326	hypothetical prote
3	51	51.0	434	2 T47545	monodehydroascorba
4	48	48.0	1135	2 T30561	scythe protein - A
5	47	47.0	1151	2 T24541	hypothetical prote
6	46.5	46.5	467	2 AH3437	DNA repair protein
7	46	46.0	178	2 E95994	hypothetical prote
8	46	46.0	198	2 S70515	hypothetical prote
9	46	46.0	198	2 S70515	hypothetical prote
10	46	46.0	198	2 S70515	hypothetical prote
11	46	46.0	437	2 C87688	cysteine string pr
12	45	45.0	1408	2 T47671	FolC bifunctional
13	45	45.0	382	2 T08301	P-glycoprotein-1lk
14	45	45.0	434	2 T00182	monodehydroascorba
15	44.5	44.5	297	2 F86839	phosphate ABC tran
16	44.5	44.5	1189	2 T51481	hypothetical prote
17	44	44.0	220	2 A75287	response regulator
18	44	44.0	297	2 F70572	hypothetical prote
19	44	44.0	624	2 T27096	hypothetical prote
20	43.5	43.5	1106	1 TVHUGL	transforming prote
21	43	43.0	304	2 T10212	hypothetical prote
22	43	43.0	99	2 A55819	nonsilence chromos
23	43	43.0	133	2 D70910	hypothetical prote
24	43	43.0	179	2 F71854	probable outer mem
25	43	43.0	220	2 E64660	peptidoglycan asso
26	43	43.0	308	2 T17946	CAMP response elem
27	43	43.0	312	2 E64072	hypothetical prote
28	43	43.0	344	2 JC5602	spermidine/putresc
29	43	43.0	344	2 JC5601	CAMP response elem

30	43	43.0	428	2 T32952	hypothetical prote
31	43	43.0	547	2 E70650	phosphoglucosylase
32	43	43.0	873	2 T16282	hypothetical prote
33	42.5	42.5	153	1 B69215	conserved hypotet
34	42.5	42.5	249	2 JH0629	cleavage signal-1
35	42	42.0	217	2 C37944	CAMP response elem
36	42	42.0	229	2 B37944	CAMP response elem
37	42	42.0	229	2 A37944	CAMP response elem
38	42	42.0	231	2 S36101	CAMP response elem
39	42	42.0	341	2 S20827	CAMP response elem
40	42	42.0	723	1 S26686	CAMP response elem
41	42	42.0	852	2 S26686	CAMP response elem
42	42	42.0	1076	2 T06310	RNA-directed RNA p
43	42	42.0	137	2 S44764	hypothetical prote
44	41	41.0	137	2 B72720	hypothetical prote
45	41	41.0	139	2 B70925	hypothetical prote
46	41	41.0	152	2 A87261	hypothetical prote
47	41	41.0	159	2 T10699	hypothetical prote
48	41	41.0	210	2 C87305	hypothetical prote
49	41	41.0	254	1 G69884	hypothetical prote
50	41	41.0	355	2 S11152	conserved hypotet
51	41	41.0	355	2 F98084	oligopeptide trans
52	41	41.0	355	2 F95220	hypothetical prote
53	41	41.0	416	1 A42879	hypothetical prote
54	41	41.0	427	2 T05019	advanced glycoyla
55	41	41.0	433	2 T06407	hypothetical prote
56	41	41.0	437	2 C35147	monodehydroascorba
57	41	41.0	438	2 D70528	integrase homolog
58	41	41.0	498	2 PC6300	hypothetical prote
59	41	41.0	542	2 E84250	acyl-CoA synthet
60	41	41.0	564	2 I53106	gene glt protein -
61	41	41.0	623	2 G72412	hypothetical prote
62	41	41.0	632	2 T46020	hypothetical prote
63	41	41.0	712	2 T44834	hypothetical prote
64	41	41.0	771	2 T02565	hypothetical prote
65	41	41.0	798	2 T33022	disease resistance
66	41	41.0	874	2 B86322	hypothetical prote
67	41	41.0	915	2 AC3477	beta14.8 protein -
68	41	41.0	1272	2 C64513	DNA mismatch repa
69	41	41.0	1286	2 H89960	hypothetical prote
70	41	41.0	1435	2 T42629	tenascin-X - bovin
71	40.5	40.5	101	2 H72556	hypothetical prote
72	40.5	40.5	272	2 B71618	mezozoite surface
73	40.5	40.5	595	1 EDBEMC	immediate-early pn
74	40.5	40.5	878	2 H83184	phosphoenolpyruvat
75	40	40.0	134	2 S23003	trac protein - Esc
76	40	40.0	198	2 A71318	hypothetical prote
77	40	40.0	249	2 B96022	probable dehydroge
78	40	40.0	276	2 T44319	hypothetical prote
79	40	40.0	278	1 TPHUTW	hypothetical prote
80	40	40.0	291	2 D64043	citronin T, slow B
81	40	40.0	306	2 T00177	hypothetical prote
82	40	40.0	306	2 G89988	hypothetical prote
83	40	40.0	327	2 T32583	hypothetical prote
84	40	40.0	335	2 S54287	hypothetical prote
85	40	40.0	339	2 G82596	othn protein - vib
86	40	40.0	346	2 S21265	phage-related prot
87	40	40.0	357	2 H82993	acetylserotonin O-
88	40	40.0	357	2 H71122	conserved hypotet
89	40	40.0	383	2 T30730	hypothetical prote
90	40	40.0	389	2 C83202	hypothetical prote
91	40	40.0	394	2 A25281	alginate biosynthe
92	40	40.0	421	2 T23981	apolipoprotein A-I
93	40	40.0	449	2 S27490	hypothetical prote
94	40	40.0	461	2 T22946	catalase (EC 1.11.
95	40	40.0	475	2 H84567	hypothetical prote
96	40	40.0	512	2 C72505	probable diacylgly
97	40	40.0	524	2 S35551	transcription fact
98	40	40.0	583	2 JH0395	DNA-binding protei
99	40	40.0	591	2 UC7657	mannan endo-1,4-be
100	40	40.0	615	2 T47395	hypothetical prote
101	40	40.0	620	2 T21449	hypothetical prote
102	40	40.0	635	2 H69626	PTS fructose-speci

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OM protein - protein search, using sw model

Run on: April 28, 2005, 17:25:43 ; Search time 93.6667 Seconds
(without alignments)
109.341 Million cell updates/sec

Title: US-10-017-168-8
Perfect score: 100
Sequence: 1 SREVEDAPKVEPASEREGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database: Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	256	083448	083448 treponema p
2	100	100.0	432	051953	051953 treponema p
3	100	100.0	548	093C44	093C44 treponema p
4	96	96.0	348	09ALV7	09ALV7 treponema p
5	96	96.0	428	09ALV6	09ALV6 treponema p
6	92	92.0	393	093CA3	093CA3 treponema p
7	73	73.0	227	083449	083449 treponema p
8	54	54.0	434	093X74	093X74 brasica ra
9	54	54.0	434	075U06	075U06 brasica ol
10	52	52.0	2192	081BW7	081BW7 plasmodium
11	51	51.0	434	1 MDA3	091f33 arabidopsis
12	49	49.0	983	06A9Z4	06A9Z4 propionibac
13	48	48.0	265	065U70	065U70 bacillus li
14	48	48.0	572	1 STR	07nm1l chromobacte
15	48	48.0	769	075BK7	075BK7 ashyba goss
16	48	48.0	1135	2 OYHD3	09yhd3 xenopus lae
17	48	48.0	1159	2 O9IMX8	09IMX8 cercopithec
18	47	47.0	612	2 O960T9	0960T9 dirosophila
19	47	47.0	612	2 O9VCA5	09VCA5 dirosophila
20	47	47.0	1165	2 O7JUP6	07JUP6 caenorhabdi
21	47	47.0	1475	2 O6CBP1	06CBP1 yarrowia li
22	46.5	46.5	294	2 O6UGG2	06UGG2 enterobacte
23	46.5	46.5	467	2 O8YFN4	08YFN4 bruceella me
24	46.5	46.5	467	2 O8G279	08G279 bruceella su
25	46	46.0	137	2 O6AHX3	06AHX3 homo sapien
26	46	46.0	142	2 O8ETU0	08ETU0 homo sapien
27	46	46.0	178	2 O92UB5	092UB5 rhizobium m
28	46	46.0	198	1 DUC5	093455 bos taurus
29	46	46.0	198	1 DUC5	093455 homo sapien
30	46	46.0	198	1 DUC5	093455 mus musculu
31	46	46.0	198	1 DUC5	093455 rictus norv

32	46	46.0	204	2	0921J3	0921J3 mus musculu
33	46	46.0	228	2	06ERF9	06ERF9 oryza sativ
34	46	46.0	261	2	09QUP7	09QUP7 mus musculu
35	46	46.0	262	2	075Z26	075Z26 sus scrofa
36	46	46.0	262	2	088346	088346 mus musculu
37	46	46.0	322	2	09D595	09D595 mus musculu
38	46	46.0	435	2	09XFE3	09XFE3 oryza sativ
39	46	46.0	435	2	0652L6	0652L6 oryza sativ
40	46	46.0	437	2	09A2L6	09A2L6 caulobacter
41	46	46.0	649	1	DXS1	092162 kitasacospo
42	46	46.0	944	2	08CGI1	08CGI1 mus musculu
43	46	46.0	1408	2	09M3B9	09M3B9 arabidopsis
44	45	45.0	136	2	08C457	08C457 mus musculu
45	45	45.0	151	2	084851	084851 oryza sativ
46	45	45.0	256	2	08WV22	08WV22 homo sapien
47	45	45.0	382	2	051988	051988 halobacteri
48	45	45.0	434	1	MDAS	042711 cucumis sat
49	45	45.0	436	2	08K0S3	08K0S3 mus musculu
50	45	45.0	477	2	093YGI	093YGI mesembryant
51	45	45.0	579	2	08QZS3	08QZS3 mus musculu
52	45	45.0	582	2	08ZFE9	08ZFE9 streptomyce
53	45	45.0	781	2	09SNG8	09SNG8 oryza sativ
54	45	45.0	850	2	07XU82	07XU82 dirosophila
55	45	45.0	943	2	P31638	P31638 dirosophila
56	45	45.0	944	2	09V862	09V862 dirosophila
57	45	45.0	1072	2	098LC1	098LC1 rhizobium 1
58	45	45.0	1247	2	0805Z8	0805Z8 cercopithec
59	44.5	44.5	267	1	SSP2	082820 homo sapien
60	44.5	44.5	297	2	09CEM6	09CEM6 lactococcus
61	44.5	44.5	357	2	08PYE8	08PYE8 xanthomonas
62	44.5	44.5	584	2	08N7H2	08N7H2 homo sapien
63	44.5	44.5	792	2	08CEY0	08CEY0 staphylococ
64	44.5	44.5	964	2	08N263	08N263 homo sapien
65	44.5	44.5	1106	2	08N1L3	08N1L3 homo sapien
66	44.5	44.5	1106	2	068DA6	068DA6 homo sapien
67	44.5	44.5	1180	2	08VYW7	08VYW7 arabidopsis
68	44.5	44.5	1189	2	09LF07	09LF07 arabidopsis
69	44.5	44.5	1256	2	08NEN5	08NEN5 homo sapien
70	44.5	44.5	1259	2	07Z7L2	07Z7L2 homo sapien
71	44.5	44.5	1325	2	096FW1	096FW1 homo sapien
72	44	44.0	130	2	09K4G3	09K4G3 streptomyce
73	44	44.0	184	2	08XYS0	08XYS0 raietonia s
74	44	44.0	220	2	09RS02	09RS02 delnoccocus
75	44	44.0	263	2	08MKH6	08MKH6 bos taurus
76	44	44.0	285	2	07PKJ6	07PKJ6 anophelis g
77	44	44.0	297	2	006189	006189 mycobacteri
78	44	44.0	297	2	07TY75	07TY75 mycobacteri
79	44	44.0	328	2	08ORS6	08ORS6 triturus ca
80	44	44.0	362	2	06AKT3	06AKT3 brachydanio
81	44	44.0	368	2	070784	070784 oat sterile
82	44	44.0	450	2	070PA4	070PA4 mellittangiu
83	44	44.0	483	2	09JGT4	09JGT4 northern ce
84	44	44.0	528	1	PGGA	096135 homo sapien
85	44	44.0	557	2	09N4H5	09N4H5 caenorhabdi
86	44	44.0	579	2	076UQ2	076UQ2 rictus norv
87	44	44.0	609	2	09W2U4	09W2U4 dirosophila
88	44	44.0	702	2	09W852	09W852 dirosophila
89	44	44.0	737	2	06XSW9	06XSW9 oryza sativ
90	44	44.0	805	2	08PSI4	08PSI4 methanosaar
91	44	44.0	840	2	07EYJ8	07EYJ8 oryza sativ
92	44	44.0	939	2	07ZTP9	07ZTP9 bacillus ce
93	44	44.0	1081	2	07SBY5	07SBY5 neustospora
94	44	44.0	1106	1	GLI1	098151 homo sapien
95	44	44.0	2414	2	09BZS0	09BZS0 homo sapien
96	44	44.0	2414	2	09HCL7	09HCL7 homo sapien
97	44	44.0	183	2	06N585	06N585 rhodospendo
98	43.5	43.5	304	2	09SVS9	09SVS9 arabidopsis
99	43.5	43.5	499	2	004376	004376 arabidopsis
100	43.5	43.5	752	2	0801W4	0801W4 brachydanio
101	43	43.0	68	2	08KRM1	08KRM1 heliobacte
102	43	43.0	68	2	06PY62	06PY62 heliobacte
103	43	43.0	68	2	06PY63	06PY63 heliobacte
104	43	43.0	68	2	06PY64	06PY64 heliobacte